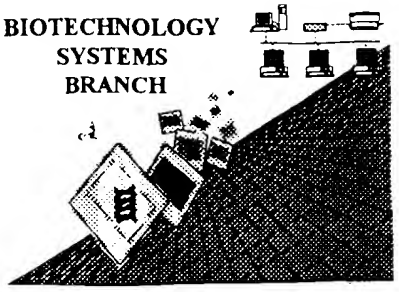
US-90
0821

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/923,830

Source: OIPE

Date Processed by STIC: 8/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/923,830

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 ____ Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4 ✓ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5 ____ Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11 ____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 ____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/923,830

DATE: 08/16/2001
TIME: 13:38:20

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I923830.raw

see item 4 on Error Summary Sheet

Does Not Comply
Corrected Diskette Needed

pgs 1-3

3 <110> APPLICANT: Nienaber, Vicki
4 Greer, Jonathan
Akad-Capatero, Celerino
Narbeck, Daniel
<120> TITLE OF INVENTION: LIGAND SCREENING AND DESIGN BY X-RAY
CRYSTALLOGRAPHY
11 <130> FILE REFERENCE: 6308.US.P1
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/923,830
C--> 13 <141> CURRENT FILING DATE: 2001-08-07
13 <150> PRIOR APPLICATION NUMBER: 09/036,184
14 <151> PRIOR FILING DATE: 1998-03-06
16 <160> NUMBER OF SEQ ID NOS: 14
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

20 <210> SEQ ID NO: 1 (global error)
21 <211> LENGTH: 51
22 <212> TYPE: DNA
23 <213> ORGANISM: Synthetic, unused - see item 10 on Error Summary
25 <400> SEQUENCE: 1
E--> 26 attaatgtcg actaaggagg tgatctaatg ttaaaatttc agtgtggcca a
27 51
29 <210> SEQ ID NO: 2 see item 1 on Error Summary Sheet
30 <211> LENGTH: 57
31 <212> TYPE: DNA
32 <213> ORGANISM: Synthetic
34 <400> SEQUENCE: 2
E--> 35 attaataagc tttcagaggg ccaggccatt ctcttccttg gtgtgactcc tgatcca
36 57
38 <210> SEQ ID NO: 3 same error
39 <211> LENGTH: 47
40 <212> TYPE: DNA
41 <213> ORGANISM: Synthetic
43 <400> SEQUENCE: 3
E--> 44 attaattgcg cagccatccc ggactataca gaccatcgcc ctgccct same
45 47
47 <210> SEQ ID NO: 4
48 <211> LENGTH: 46
49 <212> TYPE: DNA
50 <213> ORGANISM: Synthetic
52 <400> SEQUENCE: 4
E--> 53 attaatcagc tgctccggat agagatagtc ggtagactgc tctttt same
54 46
56 <210> SEQ ID NO: 5
57 <211> LENGTH: 54

see item 1 on Error Summary Sheet (global format error)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/923,830
DATE: [illegible]
TIME: [illegible]

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I923830.raw

58 <210> TYPE: DNA
59 <213> ORGANISM: Synthetic
60 <400> SEQUENCE: 5
E--> 62 attaatcagc tgaaaatgac tgttgtga same
63 <210> SEQ ID NO: 6
64 <211> LENGTH: 51
65 <212> TYPE: DNA
66 <213> ORGANISM: Synthetic
67 <400> SEQUENCE: 6
E--> 71 attaatgtcg actaaggagg tgatctaatg ttaaaatttc agtgtggcca a same
72 <210> SEQ ID NO: 7
73 <211> LENGTH: 37
74 <212> TYPE: DNA
75 <213> ORGANISM: Synthetic
76 <400> SEQUENCE: 7
E--> 80 attaatgcta gcctcgagcc accatgagag ccctgct same
81 <210> SEQ ID NO: 8
82 <211> LENGTH: 42
83 <212> TYPE: DNA
84 <213> ORGANISM: Synthetic
85 <400> SEQUENCE: 8
E--> 89 attaatgcta gcctcgagtc acttgttgtg actgcggatc ca same
90 <210> SEQ ID NO: 9
91 <211> LENGTH: 44
92 <212> TYPE: DNA
93 <213> ORGANISM: Synthetic
94 <400> SEQUENCE: 9
E--> 98 ggtggtgaat tctcccccaa taatgccttt ggagtcgctc acga same
99 <210> SEQ ID NO: 10
100 <211> LENGTH: 111
101 <212> TYPE: DNA
102 <213> ORGANISM: Yeast Pichia Pastoris
103 <400> SEQUENCE: 10
E--> 107 atgttctctc caattttgtc cttggaaatt attttagctt tggctacttt gcaatctgtc
108 <210>
E--> 109 ttcgctcagc cagttatctg cactaccgtt ggttccgctg ccgagggatc c same
110 <211>
111 <212> SEQ ID NO: 11
112 <213> LENGTH: 22
113 <400> TYPE: DNA
114 ORGANISM: Synthetic
115 SEQUENCE:
E--> 118 gaaacttcca aaagtcgcca ta same
119 22

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/923,830

DATE: [illegible]
TIME: 13:28:20

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I923830.raw

121 <210> SEQ ID NO: 12
122 <211> LENGTH: 92
123 <212> TYPE: DNA
124 <213> ORGANISM: Synthetic
126 <400> SEQUENCE: 12
E--> 127 attaatgaat tcctcgagcg gtccgggatc cctcggcagc ggaaccaacg gtagtgcaga
128 60
E--> 129 taactggctg agcgaagaca gattgcaaag ta
130 92
132 <210> SEQ ID NO: 13
133 <211> LENGTH: 46
134 <212> TYPE: DNA
135 <213> ORGANISM: Synthetic
137 <400> SEQUENCE: 13
E--> 138 attaatggat ccttggacaa gaggattatt gggggagaat tcacca
139 46
141 <210> SEQ ID NO: 14
142 <211> LENGTH: 47
143 <212> TYPE: DNA
144 <213> ORGANISM: Synthetic
146 <400> SEQUENCE: 14
E--> 147 attaatctcg agcggtccgt cacttggtgt gactgcgaat ccagggt
148 47
E--> 150 43
E--> 152 6308.us.dl
E--> 156 43
E--> 157 -
E--> 158 43
E--> 160 43

same

same

same

Delete

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/923,830

DATE: [illegible]
TIME: [illegible]

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I923830.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:[illegible] Counted:21 SEQ:1
L:35 M:254 E: No. of Bases conflict, LENGTH:Input:[illegible] Counted:37 SEQ:2
L:44 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:3
L:53 M:254 E: No. of Bases conflict, LENGTH:Input:[illegible] Counted:46 SEQ:4
L:62 M:254 E: No. of Bases conflict, LENGTH:Input:[illegible] Counted:48 SEQ:5
L:71 M:254 E: No. of Bases conflict, LENGTH:Input:[illegible] Counted:51 SEQ:6
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:7
L:89 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:8
L:98 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:9
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:10
M:284 Repeated in SeqNo=10
L:118 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:11
L:127 M:254 E: No. of Bases conflict, LENGTH:Input:[illegible] Counted:60 SEQ:12
M:284 Repeated in SeqNo=12
L:138 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:13
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:14
M:284 Repeated in SeqNo=14
L:158 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:158 M:112 C: (48) String data converted to lower case,
L:157 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:160 M:252 E: No. of Seq. differs, <211>LENGTH:Input:47 Found:53 SEQ:14